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OIPE

RAW SEQUENCE LISTING

DATE: 01/04/2002

PATENT APPLICATION: US/09/921,922A

TIME: 15:05:42

Input Set : A:\16516-107 seq listing.txt
Output Set: N:\CRF3\01042002\I921922A.raw

P5

1 <110> APPLICANT: Boronat, Albert;
 2 Campos, Narciso;
 3 Rodriguez-Concepcion, Manuel;
 4 Rohmer, Michel;
 5 Seeman, Myriam;
 6 Valentin, Henry E.;
 7 Venkatesh, Tyamagondlu V.;
 8 Venkatramesh, Mylavarampu

ENTERED

10 <120> TITLE OF INVENTION: Methyl-D-Erythritol Phosphate Pathway Genes
 12 <130> FILE REFERENCE: 16516.107/35-21(51897)US

OK >> 14 <140> CURRENT APPLICATION NUMBER: US/09/921,922A
 14 <141> CURRENT FILING DATE: 2001-12-19

14 <150> PRIOR APPLICATION NUMBER: US 60/223,483

15 <151> PRIOR FILING DATE: 2000-08-07

17 <160> NUMBER OF SEQ ID NOS: 85

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 2520

21 <212> TYPE: DNA

22 <213> ORGANISM: Arabidopsis thaliana

24 <220> FEATURE:

25 <221> NAME/KEY: CDS

26 <222> LOCATION: (154)..(2376)

28 <400> SEQUENCE: 1

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34	ctcgtcttca gttactttga ttcaactgaga aaa atg gcg act gga gta ttg cca	174
35	Met Ala Thr Gly Val Leu Pro	
36	1 5	
38	gct ccg gtt tct ggg atc aag ata ccg gat tcg aaa gtc ggg ttt ggt	222
39	Ala Pro Val Ser Gly Ile Lys Ile Pro Asp Ser Lys Val Gly Phe Gly	
40	10 15 20	
42	aaa agc atg aat ctt gtg aga att tgt gat gtt agg agt cta aga tct	270
43	Lys Ser Met Asn Leu Val Arg Ile Cys Asp Val Arg Ser Leu Arg Ser	
44	25 30 35	
46	gct agg aga aga gtt tcg gtt atc cgg aat tca aac caa ggc tct gat	318
47	Ala Arg Arg Arg Val Ser Val Ile Arg Asn Ser Asn Gln Gly Ser Asp	
48	40 45 50 55	
50	tta gct gag ctt caa cct gca tcc gaa gga agc cct ctc tta gtg cca	366
51	Leu Ala Glu Leu Gln Pro Ala Ser Glu Gly Ser Pro Leu Leu Val Pro	
52	60 65 70	
54	aga cag aaa tat tgt gaa tca ttg cat aag acg gtg aga agg aag act	414
55	Arg Gln Lys Tyr Cys Glu Ser Leu His Lys Thr Val Arg Arg Lys Thr	
56	75 80 85	
58	cgt act gtt atg gtt gga aat gtc gcc ctt gga agc gaa cat ccg ata	462
59	Arg Thr Val Met Val Gly Asn Val Ala Leu Gly Ser Glu His Pro Ile	
60	90 95 100	
62	agg att caa acg atg act act tcg gat aca aaa gat att act gga act	510

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63	Arg	Ile	Gln	Thr	Met	Thr	Thr	Ser	Asp	Thr	Lys	Asp	Ile	Thr	Gly	Thr	
64		105				110					115						
66	gtt	gat	gag	gtt	atg	aga	ata	gcg	gat	aaa	gga	gct	gat	att	gta	agg	558
67	Val	Asp	Glu	Val	Met	Arg	Ile	Ala	Asp	Lys	Gly	Ala	Asp	Ile	Val	Arg	
68	120					125					130					135	
70	ata	act	gtt	caa	ggg	aag	aaa	gag	gcg	gat	gcg	tgc	ttt	gaa	ata	aaa	606
71	Ile	Thr	Val	Gln	Gly	Lys	Lys	Glu	Ala	Asp	Ala	Cys	Phe	Glu	Ile	Lys	
72						140					145					150	
74	gat	aaa	ctc	gtt	cag	ctt	aat	tac	aat	ata	ccg	ctg	gtt	gca	gat	att	654
75	Asp	Lys	Leu	Val	Gln	Leu	Asn	Tyr	Asn	Ile	Pro	Leu	Val	Ala	Asp	Ile	
76						155					160					165	
78	cat	ttt	gcc	cct	act	gta	gcc	tta	cga	gtc	gct	gaa	tgc	ttt	gac	aag	702
79	His	Phe	Ala	Pro	Thr	Val	Ala	Leu	Arg	Val	Ala	Glu	Cys	Phe	Asp	Lys	
80						170					175					180	
82	atc	cgt	gtc	aac	cca	gga	aat	ttt	gcg	gac	agg	ccg	gcc	cag	ttt	gag	750
83	Ile	Arg	Val	Asn	Pro	Gly	Asn	Phe	Ala	Asp	Arg	Arg	Ala	Gln	Phe	Glu	
84						185					190					195	
86	acg	ata	gat	tat	aca	gaa	gat	gaa	tat	cag	aaa	gaa	ctc	cag	cat	atc	798
87	Thr	Ile	Asp	Tyr	Thr	Glu	Asp	Glu	Tyr	Gln	Lys	Glu	Leu	Gln	His	Ile	
88	200					205					210					215	
90	gag	cag	gtc	ttc	act	cct	ttg	gtt	gag	aaa	tgc	aaa	aag	tac	ggg	aga	846
91	Glu	Gln	Val	Phe	Thr	Pro	Leu	Val	Glu	Lys	Cys	Lys	Lys	Tyr	Gly	Arg	
92						220					225					230	
94	gca	atg	cgt	att	ggg	aca	aat	cat	gga	agt	ctt	tct	gac	cgt	atc	atg	894
95	Ala	Met	Arg	Ile	Gly	Thr	Asn	His	Gly	Ser	Leu	Ser	Asp	Arg	Ile	Met	
96						235					240					245	
98	agc	tat	tac	ggg	gat	tct	ccc	cga	gga	atg	gtt	gaa	tct	gcg	ttt	gag	942
99	Ser	Tyr	Tyr	Gly	Asp	Ser	Pro	Arg	Gly	Met	Val	Glu	Ser	Ala	Phe	Glu	
100						250					255					260	
102	ttt	gca	aga	ata	tgt	cgg	aaa	tta	gac	tat	cac	aac	ttt	gtt	ttc	tca	990
103	Phe	Ala	Arg	Ile	Cys	Arg	Lys	Leu	Asp	Tyr	His	Asn	Phe	Val	Phe	Ser	
104						265					270					275	
106	atg	aaa	gcg	agc	aac	cca	gtg	atc	atg	gtc	cag	gcg	tac	cgt	tta	ctt	1038
107	Met	Lys	Ala	Ser	Asn	Pro	Val	Ile	Met	Val	Gln	Ala	Tyr	Arg	Leu	Leu	
108						280					285					290	295
110	gtg	gct	gag	atg	tat	gtt	cat	gga	tgg	gat	tat	cct	ttg	cat	ttg	gga	1086
111	Val	Ala	Glu	Met	Tyr	Val	His	Gly	Trp	Asp	Tyr	Pro	Leu	His	Leu	Gly	
112						300					305					310	
114	gtt	act	gag	gca	gga	gaa	ggc	gaa	gat	gga	cg	atg	aaa	tct	gcg	att	1134
115	Val	Thr	Glu	Ala	Gly	Glu	Gly	Glu	Asp	Gly	Arg	Met	Lys	Ser	Ala	Ile	
116						315					320					325	
118	gga	att	ggg	acg	ctt	ctt	cag	gac	ggg	ctc	ggt	gac	aca	ata	aga	gtt	1182
119	Gly	Ile	Gly	Thr	Leu	Leu	Gln	Asp	Gly	Leu	Gly	Asp	Thr	Ile	Arg	Val	
120						330					335					340	
122	tca	ctg	acg	gag	cca	cca	gaa	gag	gag	ata	gat	ccc	tgc	agg	cga	ttg	1230
123	Ser	Leu	Thr	Glu	Pro	Pro	Glu	Glu	Ile	Asp	Pro	Cys	Arg	Arg	Leu		
124						345					350					355	
126	gct	aac	ctc	ggg	aca	aaa	gct	gcc	aaa	ctt	caa	caa	ggc	gca	ccg	ttt	1278
127	Ala	Asn	Leu	Gly	Thr	Lys	Ala	Ala	Lys	Leu	Gln	Gln	Gly	Ala	Pro	Phe	

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128	360	365	370	375	
130	gaa gaa aag cat agg cat tac ttt gat ttt cag cgt cgg acg ggt gat				1326
131	Glu Glu Lys His Arg His Tyr Phe Asp Phe Gln Arg Arg Thr Gly Asp				
132	380	385	390		
134	cta cct gta caa aaa gag gga gaa gag gtt gat tac aga aat gtc ctt				1374
135	Leu Pro Val Gln Lys Glu Gly Glu Val Asp Tyr Arg Asn Val Leu				
136	395	400	405		
138	cac cgt gat ggt tct gtt ctg atg tcg att tct ctg gat caa cta aag				1422
139	His Arg Asp Gly Ser Val Leu Met Ser Ile Ser Leu Asp Gln Leu Lys				
140	410	415	420		
142	gca cct gaa ctc ctc tac aga tca ctc gct aca aag ctt gtc gtg ggt				1470
143	Ala Pro Glu Leu Leu Tyr Arg Ser Leu Ala Thr Lys Leu Val Val Gly				
144	425	430	435		
146	atg cca ttc aag gat ctg gca act gtt gat tca atc tta tta aga gag				1518
147	Met Pro Phe Lys Asp Leu Ala Thr Val Asp Ser Ile Leu Leu Arg Glu				
148	440	445	450	455	
150	cta ccg cct gta gat gat caa gtg gct cgt ttg gct cta aaa cgg ttg				1566
151	Leu Pro Pro Val Asp Asp Gln Val Ala Arg Leu Ala Leu Lys Arg Leu				
152	460	465	470		
154	att gat gtc agt atg gga gtt ata gca cct tta tca gag caa cta aca				1614
155	Ile Asp Val Ser Met Gly Val Ile Ala Pro Leu Ser Glu Gln Leu Thr				
156	475	480	485		
158	aag cca ttg ccc aat gcc atg gtt ctt gtc aac ctc aag gaa cta tct				1662
159	Lys Pro Leu Pro Asn Ala Met Val Leu Val Asn Leu Lys Glu Leu Ser				
160	490	495	500		
162	ggt ggc gct tac aag ctt ctc cct gaa ggt aca cgc ttg gtt gtc tct				1710
163	Gly Gly Ala Tyr Lys Leu Leu Pro Glu Gly Thr Arg Leu Val Val Ser				
164	505	510	515		
166	cta cga ggc gat gag cct tac gag gag ctt gaa ata ctc aaa aac att				1758
167	Leu Arg Gly Asp Glu Pro Tyr Glu Glu Leu Glu Ile Leu Lys Asn Ile				
168	520	525	530	535	
170	gat gct act atg att ctc cat gat gta cct ttc act gaa gac aaa gtt				1806
171	Asp Ala Thr Met Ile Leu His Asp Val Pro Phe Thr Glu Asp Lys Val				
172	540	545	550		
174	agc aga gta cat gca gct cgg agg cta ttc gag ttc tta tcc gag aat				1854
175	Ser Arg Val His Ala Ala Arg Arg Leu Phe Glu Phe Leu Ser Glu Asn				
176	555	560	565		
178	tca gtt aac ttt cct gtt att cat cac ata aac ttc cca acc gga atc				1902
179	Ser Val Asn Phe Pro Val Ile His His Ile Asn Phe Pro Thr Gly Ile				
180	570	575	580		
182	cac aga gac gaa ttg gtg att cat gca ggg aca tat gct gga ggc ctt				1950
183	His Arg Asp Glu Leu Val Ile His Ala Gly Thr Tyr Ala Gly Gly Leu				
184	585	590	595		
186	ctt gtg gat gga cta ggt gat ggc gta atg ctc gaa gca cct gac caa				1998
187	Leu Val Asp Gly Leu Gly Asp Gly Val Met Leu Glu Ala Pro Asp Gln				
188	600	605	610	615	
190	gat ttt gat ttt ctt agg aat act tcc ttc aac tta tta caa gga tgc				2046
191	Asp Phe Asp Phe Leu Arg Asn Thr Ser Phe Asn Leu Leu Gln Gly Cys				
192	620	625	630		

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194	aga atg cgt aac act aag acg gaa tat gta tcg tgc ccg tct tgt gga	2094
195	Arg Met Arg Asn Thr Lys Thr Glu Tyr Val Ser Cys Pro Ser Cys Gly	
196	635 640 645	
198	aga acg ctt ttc gac ttg caa gaa atc acg gcc gag atc cga gaa aag	2142
199	Arg Thr Leu Phe Asp Leu Gln Glu Ile Ser Ala Glu Ile Arg Glu Lys	
200	650 655 660	
202	act tcc cat tta cct ggc gtt tcg atc gca atc atg gga tgc att gtg	2190
203	Thr Ser His Leu Pro Gly Val Ser Ile Ala Ile Met Gly Cys Ile Val	
204	665 670 675	
206	aat gga cca gga gaa atg gca gat gct gat ttc gga tat gta ggt ggt	2238
207	Asn Gly Pro Gly Glu Met Ala Asp Ala Asp Phe Gly Tyr Val Gly Gly	
208	680 685 690 695	
210	tct ccc gga aaa atc gac ctt tat gtc gga aag acg gtg gtg aag cgt	2286
211	Ser Pro Gly Lys Ile Asp Leu Tyr Val Gly Lys Thr Val Val Lys Arg	
212	700 705 710 710	
214	ggg ata gct atg acg gag gca aca gat gct ctg atc ggt ctg atc aaa	2334
215	Gly Ile Ala Met Thr Glu Ala Thr Asp Ala Leu Ile Gly Leu Ile Lys	
216	715 720 725	
218	gaa cat ggt cgt tgg gtc gac ccg ccc gtg gct gat gag tag	2376
219	Glu His Gly Arg Trp Val Asp Pro Pro Val Ala Asp Glu	
220	730 735 740	
222	atttcaaaac ggagaaagat ggggtggccca ttctttgaaa actgtgagag aagatata	2436
224	tatttgtgt tgtatatcat ctgtttgtg tgtattgtcat catcattttg aacaatgtc	2496
226	caaatactctt aagttgataa aagt	2520
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230	<211> LENGTH: 33675	
231	<212> TYPE: DNA	
232	<213> ORGANISM: Oryza sativa	
234	<220> FEATURE:	
235	<221> NAME/KEY: CDS	
236	<222> LOCATION: (6924)..(7019),(7163)..(7269),(7344)..(7444),(7525)..(7634),	
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238	<222> LOCATION: (9012)..(9071),(9163)..(9225),(9328)..(9472),(9589)..(9730),	
239	<222> LOCATION: (9951)..(10028),(10134)..(10293),(10694)..(10798),	
240	<222> LOCATION: (11028)..(11129)	
242	<220> FEATURE:	
243	<221> NAME/KEY: unsure	
244	<222> LOCATION: (1..33675)	
245	<223> OTHER INFORMATION: unsure at all n locations	
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251	ggttaacccc tccctcactt ggagattcgt gcaagcaact cgattaatgc attaatgt	120
253	tgcgttaggt ttccctacgg aagagcttag tttcgtaacg aaaaaaaccg gccacgtt	180
255	gcatcgagcc tactttaatt agcgtggaa aataattcaa agtagcgacc tgtaccctgt	240
257	ggcaacctag cgcgccgc catggctt gttccgctcg tgacagtgtct cctgttgc	300
259	ggctcatgcc tggatcagc gcccggacg acatcgccgg cggcgtccgc gggttccacg	360
261	gctgacacgtc cgtagtgcg acggccatct acaaaccctcg gctgactcg	420
263	gtcggacacc gcaacctcgc caggcaaggc gccaccggcg ggctgtcccg gtacaccacg	480
265	aggcttccct acggcgtaac cgtcgccgc gccaccggcc ggtgtccga cggctac	540

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267	atcatcgact	tcctcggtga	cgtcatcagt	ttaatttctc	tctctcttcc	gtctgaaaaaa	600
269	tggaagaaac	aatattatata	tacgttata	atatatgcgt	ttttgtttcg	gattaaattg	660
271	tggatatgt	cgatcgatgt	cgagctagag	atcttgcct	ccctctgtc	aaccgtacc	720
273	tcgacgaggg	cgcggacttc	gcccacggcg	tcaacttcgc	cgtccggc	gccaccgcgc	780
275	tcaacacgac	ggcgcgtcgcc	gccaggcgga	tcaccgtccc	ccacaccaac	agccccctcg	840
277	acgtgcagct	cagattttt	ttgtttttaga	gaagggtatt	ttttaccgg	cctctacatc	900
279	caaccggata	tatacggcta	ttgaagttagg	gaacttaacc	ctgtaaacaa	tccatccata	960
281	gaggatatga	acctaagacc	ttgaggtact	acttcaaccg	gatataacg	tgcagctcag	1020
283	atggttcaag	gaattcatga	actccacaac	tagttctct	caaggtgaac	gaacaaactg	1080
285	aaacgcattt	cagcttaatt	tcgaccgggt	cctgatcagt	gccagtcagc	aatgctgtat	1140
287	ctcacaata	attaagctaa	tgtacagctt	ttcagtgcct	gaatgactt	catatagaga	1200
289	aatcttgt	tatataatata	tactttttc	tgaaaagaaaa	aagtcttt	gtgtgagcat	1260
291	tgcattgcag	agatccgtga	aaagctgtcg	aagtcaactgg	ttatgctgg	agagatcgga	1320
293	ggaaacgact	acaactacgc	cttcctccag	acctggccga	tggacgggt	atacagcctc	1380
295	ggcaacgtca	cacgcatgat	cgaaaagcgtt	gccacggccg	tcgatctgt	accggaagtc	1440
297	gtgcagtcca	tagccagcgc	agccaaaggta	cacaccattc	ttttccatta	atttttggga	1500
299	ccttattttt	aaaataataa	tcctggctac	aaagtaatta	attaagaact	aaattaattt	1560
301	ttgtgggttt	tgtacacag	gaggtgctcg	acatgggcgc	gacgcgggt	gtgatcccg	1620
303	gcaacctccc	gtgggttgc	gtgcccagct	acatgagcgc	ggtgaacgcg	acgaccggg	1680
305	cgcgctacga	cgcgcgcgg	tgcctcgctc	cgctcaacct	cttcgcgcgc	ctgcacaacg	1740
307	cgtggctgcg	ccgcgcgcgtc	ggggagctgc	ggcgcgcgt	ccggggcgc	gcgtggctcg	1800
309	cgtacgcgga	ctactccgc	gctgtacgcgc	cgacgcgtgg	cggggcagcg	gcgcgcggcgt	1860
311	tcgacgagcg	gcgcgtgttc	agggcgtgt	gcccccaagg	cgggcggggc	gcgtacgggt	1920
313	tcgacgtgc	cgcgtgtgc	gccccgcgg	ggacggcggc	gtgcgcgcac	ccggggaggt	1980
315	acgtgagctg	ggacggcgtc	cacctgacgc	agcgcgcgt	cgccgtcat	gccgagctgc	2040
317	tgtccgcgc	ttggcctcg	cacccgcctc	cgataaattt	cacgaacagc	gcgcgcgcgt	2100
319	gaggcgggt	tgcattggctt	ggcggtttt	tctgatcaaa	actactcaag	tttgcgggt	2160
321	tttgatttat	aaataaaaacc	atatgcgatt	ttgctaaacg	tttgcgcgt	gatttcttt	2220
323	cggaagaaaa	aatctcaccc	gagtgtatgca	tagcgggtcc	caaccatatg	tgccctgacc	2280
325	tttctctgt	tccttcgcgt	cgtgcactga	caacccatcaca	gtatgtttt	ggtatggcg	2340
327	tttgcggccc	aactcaatct	gtaatacatt	gggctgtcg	attgggttt	ttggacttca	2400
329	tagactggat	cggagaaagt	tgggtatatt	acttttcat	ttttgtata	aaatgattaa	2460
331	ttaaacagtc	taggataatt	actgttagact	ctaataatat	tgtttggta	agtattatta	2520
333	tacattcctg	tatttgacac	tctaagagca	tggccaagag	ttgcctgaaa	gtctcttc	2580
335	aaatctgcct	ttcattctct	aatgagaatt	taaggattaa	aaatataactt	atttcaata	2640
337	gacagcataa	attnaattcc	ctagaataaa	aaaatgc	cctaacaaca	gaaatttagat	2700
339	tcctctaccc	gcacccatc	agatcgctcg	attnaagatc	acgcacatct	acaccgcct	2760
341	cccgctcgct	tttctctagt	gtgggagct	cgcgtcaag	agacggaaat	cgggacaacag	2820
343	aatgattcc	agcttagcga	aatgaaagg	gaagacat	gtcataccta	caccacata	2880
345	agtatgcct	agcacaagg	atgaaaacgg	atcgaaaacg	gatggaaact	agctttatca	2940
347	tattcggtt	cattttttt	tcggaatcg	attcgaaatc	aaaaactcgg	atacggaaat	3000
349	aaaattgaat	attatcgaaat	acagatcgg	agcgaatata	agatggaaac	aatacagtag	3060
351	cgaatattta	ccggtatata	aaaaacccct	caaatttgat	ttcttgat	agaaagagat	3120
353	atcgcttatt	attnatgtt	aatatctcca	acatttat	cgtcaat	ttatagacgg	3180
355	ccacaatcg	atgtgaaaat	cgatttcat	ggttgcct	ctaagagatc	cataatgc	3240
357	tatgattatc	attnatctt	ccaagacctt	ttacttagat	tataactt	ttaccattgc	3300
359	ataaaattgga	gatgttattt	attnatcttc	acatcttcga	aacttgaat	gtatgtat	3360
361	tactttaat	gttcaagt	acaaatgtt	taaactacaa	agtggtagat	cccggtgagc	3420
363	tctacaactt	tgtatggaa	cacatctcca	tcatgtcg	tttgaattgt	agatctgaga	3480

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/921,922A

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1950 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:2064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:2219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:2310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:2606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:2667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:2834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43